AMENDMENTS TO THE SPECIFICATION

At page 1 of the specification, under the title, please insert the following section:

CROSS-REFERENCE TO RELATED APPLICATIONS

This is a Divisional of U.S. Application No. 09/547,788, filed April 12, 2000, which claims priority from U.S. Provisional Application No. 60/128,860, filed April 12, 1999. The contents of these applications are incorporated herein by reference.

Please amend the paragraph beginning on page 12, line 17 as follows:

--In the context of amino acid sequence comparisons, the term "identity" is used to express the percentage of amino acid residues at the same relative positions that are the same. Also in this context, the term "homology" is used to express the percentage of amino acid residues at the same relative positions that are either identical or are similar, using the conserved amino acid criteria of BLAST analysis, as is generally understood in the art. For example, % identity values may be generated by WU-BLAST-2 (Altschul et al., 1996, Methods in Enzymology 266:460-480; available at [http://] "blast.wustl/edu/blast/README.html"). Further details regarding amino acid substitutions, which are considered conservative under such criteria, are provided below.--

Please amend the paragraph beginning on page 15, line 24 as follows:

--One embodiment of a 30P3C8 polynucleotide is a 30P3C8 polynucleotide having the sequence shown in FIGS. 1A-1D (SEQ ID NO: 1). A 30P3C8 polynucleotide may comprise a polynucleotide having the nucleotide sequence of human 30P3C8 as shown in FIGS. 1A-1D (SEQ ID NO: 1), wherein T can also be U; a polynucleotide that encodes all or part of the 30P3C8 protein; a sequence complementary to the foregoing; or a polynucleotide fragment of any of the foregoing. Another embodiment comprises a polynucleotide having the sequence as shown in FIGS. 1A-1D (SEQ ID NO: 1), from nucleotide residue number 165 through nucleotide residue number 1367, from residue number 165 to residue number 251 or from residue number 3 through

residue number 164 or from residue number 161 through residue number 1367, wherein T can also be U. Another embodiment comprises a polynucleotide encoding a 30P3C8 polypeptide whose sequence is encoded by the cDNA contained in the plasmid 30P3C8-GTA4 as deposited with American Type Tissue Culture Collection, Manassas, VA 20110, on January 28, 1999, as Designation/Accession No. 207083, in accordance with the requirements of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure. Another embodiment comprises a polynucleotide that is capable of hybridizing under stringent hybridization conditions to the human 30P3C8 cDNA shown in FIGS. 1A-1D (SEQ ID NO: 1) or to a polynucleotide fragment thereof.--

Please amend the paragraph beginning on page 30, line 1 as follows:

--As discussed above, redundancy in the genetic code permits variation in 30P3C8 gene sequences. In particular, one skilled in the art will recognize specific codon preferences by a specific host species and can adapt the disclosed sequence as preferred for a desired host. For example, preferred codon sequences typically have rare codons (i.e., codons having a usage frequency of less than about 20% in known sequences of the desired host) replaced with higher frequency codons. Codon preferences for a specific organism may be calculated, for example, by utilizing codon usage table available on the Internet at the following http address: [http://]www.dna.affrc.go.jp/~nakamura/codon.html. Nucleotide sequences that have been optimized for a particular host species by replacing any codons having a usage frequency of less than about 20% are referred to herein as "codon optimized sequences."--